

REMARKS

The purpose of this Preliminary Amendment is to eliminate multiple dependent claims in order to avoid the additional fee. Applicants reserve the right to reintroduce claims to canceled combined subject matter.

Attached hereto is a marked-up version of the changes made to the claims by the current amendment. The attached pages are captioned "**Version With Markings to Show Changes Made**".

Respectfully submitted,



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VERSION TO SHOW MARKINGS WITH CHANGES MADE

Claims 4,5,8,9 and 11 - 15 were amended as follows:

4. (Amended) Method according to one of claims 1 to 3, characterized by the following further step:
 - k) addition to the characteristic information of the particular homologous biosequences which is to be assigned to the potentially important species sequences by acquisition of references (links) relating to the biosequences acquired according to step f) in the second databank to at least one third databank and acquisition of the information stored in the third databank on the biosequences mentioned.
5. (Amended) Method according to one of claims 1 to 4, characterized in that the third databank holds ready a classification organized taxonomically at least in part regions.
8. (Amended) Method according to claim 2 and one of the claims referring back to claim 2, characterized in that the comparison of a given (classified) list of keywords is carried out at least with the Medical Subject Headings of the Medline Databank.
9. (Amended) Method according to one of claims 1 to 4, characterized in that the third databank is the UNIGENE databank.
11. (Amended) Method according to claim 1 or 2, characterized in that further databanks are searched for linking members to the citation determined in the third databank, and addition of the corresponding further information or of references to the further information to the corresponding species sequences of increased importance.
12. (Amended) Method according to one of claims 1 to 11, characterized in that at least the second databank is a databank accessible to the public.

13. (Amended) Method according to ~~one of claims 5 to 12~~, characterized in that the further databanks are chosen from the group consisting of the Unigene, Genemap and GDB (new) and OMIM, KEGG and UMLS databanks.

14. (Amended) Method according to ~~one of claims 1 to 13~~, characterized in that the addition of further information to the species sequences determined according to step f is carried out in a pipeline method, the information added being in the form of linking members to the assigned positions in further databanks.

15. (Amended) Method according to ~~one of claims 1 to 14~~, characterized in that the species of interest is the human species, and in that the assigned group of biosequences comprises the biosequences of invertebrate animals, mammals, primates, rodents and vertebrates, and the not yet classified new entries of the second databank.